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synthase adj II and delta-9 and factor adj a and factor adj b	4

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result set*DB=USPT,DWPI; PLUR=YES; OP=OR*

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<u>L6</u>	L1 and beta adj ketoacyl and delta-9	0	<u>L6</u>

*DB=USPT; PLUR=YES; OP=OR*

<u>L5</u>	L1 and beta adj ketoacyl and delta-9	0	<u>L5</u>
<u>L4</u>	L1 and beta adj ketoacyl and delta-9 adj desaturase	0	<u>L4</u>
<u>L3</u>	L1 and KAS and delta-9 adj desaturase	0	<u>L3</u>
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<u>L1</u>	5723595	1	<u>L1</u>

LOCUS S77464 416 aa linear BCT 20-JUN-2000  
 DEFINITION 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) beta chain  
 - Synechocystis sp. (strain PCC 6803).  
 ACCESSION S77464  
 VERSION S77464 GI:7433748  
 DBSOURCE pir: locus S77464;

summary: #length 416 #molecular-weight 44004 #checksum 1268  
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 genetic: #gene fabF  
 ;  
 superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I;  
 3-oxoacyl-[acyl-carrier-protein] synthase I homology  
 ;  
 PIR dates: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change  
 20-Jun-2000

KEYWORDS acyltransferase; fatty acid biosynthesis.  
 SOURCE Synechocystis sp.  
 ORGANISM Synechocystis sp.  
 Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 REFERENCE 1 (residues 1 to 416)  
 AUTHORS Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y.,  
 Miyajima,N., Hirosawa,M., Sugiura,M., Sasamoto,S., Kimura,T.,  
 Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K.,  
 Okumura,S., Shimpo,S., Takeuchi,C., Wada,T., Watanabe,A.,  
 Yamada,M., Yasuda,M. and Tabata,S.  
 TITLE Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions  
 JOURNAL DNA Res. 3 (3), 109-136 (1996)  
 MEDLINE 97061201

FEATURES Location/Qualifiers  
 source 1..416  
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 protein sll1069"  
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 homology #label OAS"  
 Site 167  
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 /note="Cys"

ORIGIN  
 1 manlekkrvv vtglgaitpi gntlqdywqg lmegrngigp itrfdasdqa crfggevkdf  
 61 datqfldrke akrmdrfchf avcasqqain daklvineln adeigvligt gigglkvled  
 121 qqtilldkgp srcspfmipm mianmasglt ainlgakgpn nctvtacaag snaigdafrl  
 181 vqngyakami cggteaaitp lsyagfasar alsfrnddpl hasrpfdkdr dgfvmgegsg  
 241 ilileelesa largakiyge mvgyamtcda yhitapvpdg rgatraiawa lkdsghlpem  
 301 vsyinahgts tpandvtetr aikqalgnha yniavsstks mtghllggsg gieavatvma  
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